Description

Mutated Alkaline Cellulases

Technical Field

The present invention relates to mutated alkaline cellulases which can be incorporated in laundry detergents or the like.

Background Art

When a laundry detergent is used for washing laundry, the pH of the washing liquid is mostly from 10 to 11; i.e., within an alkaline range. Therefore, an enzyme to be incorporated into laundry detergents is required to exhibit an optimum pH in an alkaline region and to be stable under an alkaline condition.

Conventionally known alkaline cellulases which can be incorporated into laundry detergents or other detergents include alkaline cellulase derived from *Bacillus* sp. KSM-635 belonging to *Bacillus* (Japanese Patent Publication (*kokoku*) No. 60-23158, Japanese Patent Publication (*kokoku*) No. 6-030578, US Patent No. 4945053, etc.); alkaline cellulase derived from *Bacillus* sp. KSM-64 (Shikata *et al. Agric. Biol. Chem.*, *54*, 91-96, 1990, Sumitomo *et al.*, *Biosci. Biotechnol. Biochem.*, *56*, 872-877, 1992); heat-resistant alkaline cellulase produced from mesophilic and alkaliphilic fungi, *Bacillus* sp. KSM-S237 (FERM-BP7875: deposited on February 6th,

1997 with Independent Administrative Institution of National Institute of Advanced Industrial Science and Technology, International Patent Organism Depositary (Tsukuba Central 6, 1-1-1 Higashi, Tsukuba, Ibaraki, Japan (postal code 305-8566))) (Japanese Patent Application Laid-Open (*kokai*) No. 10-313859); alkaline cellulase derived from *Bacillus* sp. KSM-N257 (Japanese Patent Application No. 12-281378); and alkaline cellulase derived from *Bacillus* sp. KSM-N131 (Japanese Patent Application No. 12-373859). However, in the case where the substrate is carboxymethylcellulose (CMC) these alkaline cellulases exhibit an optimum reaction pH of about 9; therefore, the cellulases do not have the optimum pH under conditions encountered during laundry washing.

In the meanshile, a study has been done on changing the optimum reaction pH of a glucosidase. The study shows that the optimum pH of a glucosidase is shifted from alkali to neutral by constructing a chimeric protein from an alkaline cellulase (NK1) derived from alkaliphilic *Bacillus* and neutral cellulase (BSC) derived from *Bacillus subtilis* (Park *et al.*, *Protein Eng.*, 6, 921-926, 1993).

Recently, it has been reported that the optimum pH of cellobiohydrolase (Cel7A) derived from *Trichoderma reesei* was increased as compared with that of its wild-type strain by substitution of amino acid residues in the vicinity of its active center (Beker *et al*, *Biochem. J.*, *356*, 19-31, 2001). However, in this case, the optimum pH of the wild-type enzyme falls within an acidic range, and the increase in the optimum

pH of the mutant is within 1 pH unit or less.

Thus, there has been substantially no report in which the optimum reaction pH of glucosidase is shifted toward the alkaline side.

The present invention is directed to the provision of a mutated alkaline cellulase having an optimum pH as an enzyme to be incorporated into detergent, which is obtained by modifying the alkaline cellulase gene.

Disclosure of the Invention

The present inventors have searched enzymes which can attain the above purpose by estimating the three-dimensional structure of an alkaline cellulase having an amino acid sequence represented by SEQ ID NO: 1 (Egl-237); in particular, the structure of its active domain, and by incorporating mutations through site-specific mutation. As a result, the present inventors have found that the optimum reaction pH in the CMC decomposition activity can be increased by deleting amino acid residues in a specific region which forms a portion of the loop structure and inserting a peptide into the position.

Accordingly, the present invention provides a mutated alkaline cellulase obtained by deleting, from a cellulase having an amino acid sequence represented by SEQ ID NO: 1 or an amino acid sequence exhibiting at least 90% homology therewith, one or more amino acid residues chosen from the 343rd to 377th positions in SEQ ID NO: 1 or from

corresponding positions, and inserting a peptide having 2 to 15 amino acid residues into at least one of the deleted positions; as well as a gene encoding the mutated alkaline cellulase.

The present invention also provides a vector containing the gene, and a transformant containing the vector.

Brief Description of the Drawings

Figs. 1a to 1c show aligned amino acid sequences of cellulases having at least 90% homology with the amino acid sequence represented by SEQ ID NO: 1.

Fig. 2 shows the optimum reaction pH of the alkaline cellulase which has been mutated through use of alanine-glycine-alanine.

Fig. 3 shows the optimum reaction pH of the alkaline cellulase which has been mutated through use of alanine-histidine-alanine.

Fig. 4 shows the optimum reaction pH of the alkaline cellulase which has been mutated through use of alanine-arginine-alanine.

Best Mode for Carrying Out the Invention

The mutated alkaline cellulases according to the present invention are obtained by using, as a cellulase to be mutated (hereinafter may be referred to as "parent alkaline cellulase"), a cellulase having an amino acid sequence represented by SEQ ID NO: 1 or an amino acid sequence

exhibiting at least 90% homology therewith, and by deleting one or more amino acid residues chosen from the 343rd to 377th positions in SEQ ID NO: 1 or from corresponding positions and inserting a peptide having 2 to 15 amino acid residues into at least one of the deleted positions. The parent alkaline cellulases may be obtained either through spontaneous or artificial mutation of the cellulase having the amino acid sequence of SEQ ID NO: 1.

The parent cellulase exhibiting 90% or more homology With the amino acid sequence represented by SEQ ID NO: 1 preferably exhibits 95% or more homology, more preferably 98% or more homology, with the amino acid sequence. The cellulase may be of wild-type or a mutant of a wild-type cellulase. The homology of an amino acid sequence can be calculated by means of a program such as maximum matching or search homology of GENETYX-WIN (Software Development Co.).

When the molecular structure of the cellulase exhibiting 90% or more homology with the amino acid sequence represented by SEQ ID NO: 1 is estimated through a homology modeling technique and by means of 3D-1D, XPLORE, and PROCHECK programs, the cellulase preferably has the following two characteristics; (i) the cellulase has an amino acid sequence exhibiting 70% or more homology, more preferably 80% or more homology, much more preferably 90% or more homology, still more preferably 95% or more homology, yet still more preferably 98% or more homology, with the region from the 42nd position (leucine) to the 404th position (valine) (i.e.,

the active domain region) (i.e., the active domain region) of SEQ ID NO: 1; and (ii) the region from the 343rd position (asparagine) to the 377th position (leucine) of SEQ ID NO: 1 has a loop structure in the cellulase molecule. The homology of an amino acid sequence may be calculated in accordance with, for example, the Lipman-Pearson method (*Science*, *227*, 1435, 1985).

In addition, the parent alkaline cellulase preferably has characteristics such as the followings: having a molecular weight of 86,000 ± 2,000 as measured through sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) or gel filtration; having an optimum reaction pH of from 7.5 to 9.0 in the case where the substrate is carboxymethylcellulose; and having an optimum reaction temperature falling within a range of from 40 to 50°C. In addition, it is preferable that the parent alkaline cellulase effectively digests lichenan as well as carboxymethylcellulose and sufficiently maintains a stability when treated at pH 9 and at 50°C for 10 minutes.

More preferably, the parent alkaline cellulase has the following characteristics: having a molecular weight of 86,000 ± 2,000 (as measured through SDS-PAGE or gel filtration employing a Sephacryl S200 column); having an optimum reaction pH of from 8.6 to 9.0 and an optimum reaction temperature of 50°C; effectively digesting lichenan as well as carboxymethylcellulose; exhibiting a remaining activity of 95% or more, where the remaining activity after

treatment at 30°C for 10 minutes is taken as 100%, after being treated at pH 9 and 50°C for 10 minutes in the presence of 5mM calcium chloride.

Accordingly, the parent alkaline cellulase of the present invention is preferably, in addition to the alkaline cellulase having the amino acid sequence represented by SEQ ID NO: 1, an alkaline cellulase having (i) the above amino acid sequence features——i.e., having a high homology in the active domain region of SEQ ID NO: 1 and containing a particular region having a loop structure in the cellulase molecule as described above——and/or the above enzymatic characteristics (particularly preferably, having the amino acid sequence features and the enzymatic characteristics in combination), and (ii) an amino acid sequence exhibiting 90% or more homology (preferably 95% or more homology, much more preferably 98% or more homology) with that represented by SEQ ID NO: 1.

Examples of the parent alkaline cellulase of the present invention include Egl-237 [derived from *Bacillus* sp. KSM-S237 (FERM BP-7875), which is "an alkaline cellulase having the amino acid sequence represented by SEQ ID NO: 1," Hakamada *et al.*, *Biosci. Biotechnol. Biochem.*, *64*, 2281-2289, 2000]; alkaline cellulases derived from *Bacillus* sp. strain 1139 (Egl-1139) (Fukumori *et al.*, *J. Gen. Microbiol.*, *132*, 2329-2335) (homology: 91.4%); alkaline cellulases derived from *Bacillus* sp. strain KSM-64 (Egl-64) (Sumitomo *et al.*, *Biosci. Biotechnol. Biochem.*, *56*, 872-877, 1992) (homology:

91.9%); and cellulases derived from *Bacillus* sp. strain KSM-N131 (Egl-N131b) (Japanese Patent Application No. 2000-47237) (homology: 95.0%).

The mutated alkaline cellulase of the present invention is obtained by deleting, from the parent alkaline cellulase, one or more amino acid residues chosen from the 343rd to 377th positions in SEQ ID NO: 1 or from corresponding positions and inserting a peptide having 2 to 15 amino acid residues into at least one of the deleted positions.

The amino acid residue(s) to be deleted may be any of 35 amino acid residues included in the 343rd to 377th positions of SEQ ID NO: 1. The number of the amino acid residue(s) to be deleted may be any of 1 to 35. The amino acid residues to be deleted are continuous or non-continuous. The amino acid residue(s) to be deleted is(are) preferably included in the 350th to 377th positions, more preferably in the 355th to 365th positions, much more preferably in the 357th to 362nd positions, of SEQ ID NO: 1.

More preferably, the amino acid residue(s) to be deleted is(are) any 1 to 27 residues, any 2 to 15 residues, or any 3 to 10 residues contained in the 343rd to 377th positions; any 1 to 8 residues, any 3 to 6 residues, or all the amino acid residues contained in the 355th to 377th positions; and any 2 residues, any 2 to 5 residues, or all the amino acid residues contained in the 357th to 362nd positions.

Three-dimensional structural analysis through homology

modeling (Ozawa *et al.*, *Protein Eng.*, *14*, 501-504, 2001) suggests that the amino acid region at the 343rd to 377th positions of SEQ ID NO: 1 is located relatively distant from the active center of Egl-237 and therefore has a high degree of freedom, and is suggested to be a region that forms a portion of the loop structure that is intimately involved in maintaining the cellulase structure.

The "amino acid residue corresponding to the 343rd to 377th positions of SEQ ID NO: 1" can be identified by comparing amino acid sequences by means of a known algorithm such as Lipman-Pearson's method, and aligning the amino acid residues contained in the amino acid sequences of the alkaline cellulases such that the homology of each amino acid sequence with respect to that of SEQ ID NO: 1 is maximized. By aligning the amino acid sequence of the cellulase in such a manner, the position of the homologous amino acid residue in the amino acid sequence of each cellulase can be determined, irrespective of insertion or deletion in the amino acid sequence (Fig. 1). The homologous position is presumed to exist at the same three-dimensional position and to bring about similar effects with regard to a specific function of the target cellulase.

Table 1 shows the positions of Egl-1139, Egl-64, and Egl-N131b corresponding to the 357th to 362nd positions of alkaline cellulase having an amino acid sequence represented by SEQ ID NO: 1 (Egl-237).

Table 1

Egl-237	Egl-1139	Egl-64	Egl-N131b
357Gly	357Gly	357Gly	343Gly
358Lys	358Lys	358Lys	344Lys
359Ser	359Ser	359Ser	345Ser
360Asn	360Asn	360Asn	346Asn
361Ala	361Ala	361Ala	347Ala
362Thr	362Thr	362Thr	348Thr

The peptide to be inserted into the deleted position(s) may be formed of any of 20 essential amino acids. The peptide preferably contains alanine, glycine, histidine, or arginine. More preferably, the peptide contains alanine and glycine, alanine and histidine, or alanine and arginine.

The number of the amino acid residues forming the peptide to be inserted is preferably from 2 to 15, more preferably from 2 to 10, much more preferably from 2 to 6, particularly preferably 3.

Preferred examples of the peptide to be inserted include asparagine-threonine-alanine-valine-glycine-isoleucine, alanine-serine-methionine-leucine-phenylalanine-glutamic acid, cysteine-leucine-glycine-histidine-serine, tyrosine-glutamine-lysine-alanine-alanine, aspartic acid-methionine-isoleucine-valine, isoleucine-threonine-proline-lysine, glycine-leucine-cysteine, and serine-valine-phenylalanine, *inter alia*, a peptide containing alanine residues at both ends thereof and having 3 to 6 residues;

more preferably alanine-any one amino acid-alanine; even more preferably alanine-glycine-alanine, alanine-histidine-alanine, or alanine-arginine-alanine.

The mutated alkaline cellulases of the present invention encompasses those having one to several amino acid residues deleted, replaced, or added at position(s) in the amino acid sequence other than the mutated position(s) described above, so far as they do not lose their alkaline cellulase activity and the modified characteristics described above.

The mutated alkaline cellulase of the present invention may be obtained through incorporating a desired mutation into a parent alkaline cellulase in a manner, for example, described below.

Specifically, a parent alkaline cellulase is cultured, and the resultant culture broth is centrifuged, to thereby isolate cells. Through use of the alkaline cellulase gene collected from the cells, a chromosomal DNA containing the alkali cellulase gene is prepared [through, for example, a method of Marmar (*J. Mol. Biol.*, *3*, 208-212, 1961) or a method of Saito and Miura (*Biochim. Biophys. Acta*, *72*, 619-629, 1963)]. The chromosomal DNA may be subjected to cloning through shotgun cloning or PCR, to thereby prepare a gene (SEQ ID NO: 2) encoding the parent alkaline cellulase (e.g., alkaline cellulase having an amino acid sequence represented by SEQ ID NO: 1). To the thus-obtained gene, a mutation is introduced, and the resultant mutated gene is incorporated to

a plasmid. Appropriate host cells are transformed through use of the plasmid and then cultured, and the mutated alkaline cellulase of the present invention may be collected from the culture.

Examples of the method which may be employed to introduce a mutation into a gene encoding a parent alkaline cellulase, include site-specific mutation. For example, a Site-Directed Mutagenesis System Mutan-Super Express Km kit (product of Takara) may be used. The mutated alkaline cellulase gene may be incorporated into an appropriate vector.

The vector may be any vector which satisfies the following three conditions: (i) the vector can be replicated and maintained in host cells; (ii) the vector allows expression of the alkaline cellulase gene; and (iii) the vector can stably maintain the gene incorporated therein. When the host cell is a bacterium belonging to *Bacillus*, examples of the vector to be used include pUB110 and pHY300PLK. When the host cell is E. Coli, examples of the vector to be used include pUC18, pUC19, pBR322, and pHY300PLK.

Transformation of the host bacteria through use of the thus-obtained recombinant vector may be carried out through, for example, the protoplast method, the competent cell method, or the electroporation. Examples of the host bacteria include, but are not limited to, gram-positive bacteria such as those belonging to *Bacillus* sp. (*Bacillus subtilis*), gram-negative bacteria such as *Escherichia coli*, fungi such as those belonging to *Streptomyces* (Actinomycetes), to

Saccharomyces (yeast), and to *Aspergillus* (molds).

The thus-obtained transformant may be cultured under proper conditions using a medium containing an assimilable carbon source, nitrogen source, metal salt, vitamin, etc. The enzyme is isolated from the thus-obtained culture broth and then purified through a routine method, followed by lyophilization, spray drying, or crystallization to obtain the enzyme in a desired form.

The thus-obtained mutated alkaline cellulase has an optimum reaction pH higher than that of the parent alkaline cellulase. The optimum reaction pH lies preferably within 9.0 to 9.5, more preferably within 9.5 to as high as 10.0. In addition, other than the optimum reaction pH, the mutated alkaline cellulase preferably has the same characteristics as the parent alkaline cellulase.

Examples

Example 1 Modification of loop region of Egl-237

The molecule model of Egl-237 was constructed through homology modeling based on the analytical data of CelK, whose crystal structure had already been analyzed. Details of the model structure were determined by means of 3D-1D, XPLORE, and PROCHECK programs. Thereafter, on the basis of the obtained data, amino acid residues contained in a portion of the loop structure (from the 357th (glycine) to 362nd (threonine)) were deleted, and one of alanine-glycine-alanine, alanine-histidine-alanine, and alanine-arginine-alanine was

inserted to the deleted position. Mutation of the loop region was performed through use of mutation introducing primers 1, 2, and 3 (SEQ ID NOs: 3, 4, and 5), respectively, and through use of mutation introducing primer 4 (SEQ ID NO: 6) as an antisense primer. When alanine-glycine-alanine was inserted for mutation, Egl-237 gene was incorporated into pHY300PLK, and the product was employed as a template DNA. When alanine-histidine-alanine or alanine-arginine-alanine was inserted for mutation, a plasmid composed of pHY300PLK containing a gene mutated by alanine-glycine-alanine was employed as a template DNA. Specifically, after mixing of 0.5 μL (10 ng) of the template DNA plasmid, 20 μL (1 μM) of the mutation introducing primer, 20 μL (1 μM) of the antisense primer, 10 μL of a ×10 PCR buffer solution, 8 μL of a 10mM deoxynucleotide triphosphate (dNTP) mixture, 0.5 μL (2.5 units) of "*Pyrobest* DNA polymerase" (product of Takara), and 39.5 μL of deionized water, PCR was carried out by "gene amp PCR system 9700" (product of Amersham-Pharmacia). The reaction conditions were as follows; starting with thermal denaturation at 94°C for 2 minutes; followed by 30 cycles of 94°C for 1 minute; 60°C for 1 minute; 72°C for 1.5 minutes; and finally 72°C for 3 minutes. After purification of the resultant PCR product by "GFX PCR DNA and Gel Band Purification Kit" (Amersham-Pharmacia) (43.5 μL), 5.5 μL of a ×10 phosphorylation buffer and 1 μL (10 units) of polynucleotide kinase were added to the solution, and it was maintained at 37°C for 1 hour for phosphorylation, followed

by purification. After mixing 25 μL of the phosphorylated PCR product with 2 μL (20 ng) of the template plasmid, 10 μL of a ×10 PCR buffer, 8 μL of a 10mM dNTP mixture, 1 μL (5 units) of "*Pyrobest* DNA polymerase," and 54 μL of deionized water, PCR was conducted. The reaction conditions were as follows; starting with thermal denaturation at 94°C for 2 minutes; followed by 30 cycles of 94°C for 1 minute; 58°C for 1 minute; 72°C for 6 minutes; and finally 72°C for 12 minutes. The resultant PCR product was purified (43.5 μL). Then, 5.5 μL of a ×10 phosphorylation buffer and 1 μL (10 units) of polynucleotide kinase were added thereto, and phosphorylation was conducted at 37°C for 1 hour. The mixture was subjected to ethanol precipitation. The thus-collected DNA solution (10 μL) was subjected to ligation at 16°C for 18 hours by use of a ligation kit ver. 2 (product of Takara) for self ring closure, followed by another round of ethanol precipitation, whereby the DNA mixture was collected.

Example 2 Method for transformation

By use of 5 μL of the DNA mixture obtained in Example 1, the DNA was introduced into the *Bacillus subtilis* strain ISW1214, whereby the corresponding transformant was obtained (Chang and Cohen, *Mol. Gen. Gent.*, *168*, 111, 1979). The thus-obtained protoplast was inoculated onto a DM3 regeneration agar medium [0.8% (w/v) agar (product of Wako Pure Chemicals), 0.3M disodium succinate 6 hydrate, 0.5% "Casamino Acids Technical" (product of Difco), 0.5% yeast extract, 0.35% KH_2PO_4, 0.15% K_2HPO_4, 0.5% glucose, 0.4%

$MgCl_2 \cdot 6H_2O$, 0.01% bovine serum albumin (product of Sigma), 0.5% CMC (Kanto Chemical Co., Inc.), 0.005% trypan blue (product of Merck), and an amino acid mixture (leucine and methionine, 10 μg/mL)] containing tetracycline (15 μg/mL, Sigma), and incubated at 30°C for 72 hours to obtain a transformant. The transformant that formd a halo on the DM3 regeneration agar plate was cultured while shaking at 30°C for 15 hours in a polypeptone medium (3% polypeptone S, 3% maltose, 0.5% fish meat extract (product of Wako Pure Chemicals), 0.1% yeast extract, 0.1% KH_2PO_4, and 0.02% $MgSO_4 \cdot 7H_2O$) containing tetracycline (15 μg/mL). After collection of the cells, plasmids were extracted and purified by "Micro Prep Plasmid Purification kit" (product of Amersham-Pharmacia). The mutated nucleotide sequence of the cellulase gene, which had been inserted into the plasmids, was confirmed by means of "377DNA Sequencer" (product of Applied Biosystems). The nucleotide sequencing was performed through use of primers which were suitable for determining nucleotide sequences in the vicinity of the mutated position, and screening was performed, whereby plasmids to which the target mutation had been incorporated were obtained.

Example 3 Production of cellulase mutant

The host bacteria *B. Subtilis* strain ISW1214 was cultured at 30°C for 72 hours in a medium containing 3% polypepton S (product of Nihon Pharmaceutical), 0.5% fish meat extract, 0.05% yeast extract, 0.1% KH_2PO_4, 0.02% $MgSO_4 \cdot 7H_2O$, tetracycline (15 μg/mL), and 5% maltose.

After completion of culturing of various cellulase mutants, the cellulase activity of variants having a loop structure mutated by alanine-glycine-alanine, alanine-histidine-alanine, and alanine-arginine-alanine were found as 36800 U/L, 34700 U/L, and 32400 U/L, respectively.

The cellulase activity was determined through the 3,5-dinitrosalicylic acid (DNS) method.

That is, to a reaction mixture composed of 0.2 mL of a 0.5M glycine-sodium hydroxide buffer (pH 9.0), 0.4 mL of 2.5% (w/v) carboxymethyl cellulose (A01MC: Nippon Paper Industries), and 0.3 mL of deionized water, 0.1 mL of a properly diluted enzyme solution was added. After the resultant mixture was allowed to undergo reaction at 40°C for 20 minutes, 1 mL of a dinitrosalicylic acid reagent (0.5% dinitrosalicylic acid, 30% Rochelle Salt, 1.6% aqueous sodium hydroxide) was added, and the color of a reducing sugar was developed in boiling water for 5 minutes. After quenching in ice water, 4 mL of deionized water was added, and absorbance at 535 nm was measured to determine the production amount of the reducing sugar. A blank sample was prepared as follows; dinitrosalicylic acid reagent was added to the reaction mixture that had been treated as described except the addition of the enzyme solution. Then the enzyme solution was added thereto, and the color was developed in the same way. One unit (1 U) of an enzyme activity was defined as an amount of enzyme which produces a reducing sugar in an amount equivalent to 1 μmol of glucose in 1 minute under the above-

described reaction conditions.

Example 4 Purification of recombinant loop-modified cellulase

The supernatant of the culture broth containing the recombinant loop-modified cellulase was diluted 10-fold with deionized water, and the diluted supernatant was incorporated into a column (2.5 cm × 5 cm) containing DEAE Toyopearl (Tosoh Corporation) that had been pre-equilibrated with 10mM Tris-HCl buffer (pH 8.0). The column was washed further with the buffer, and protein was eluted with a linear gradient of from 0 to 0.4M solution of sodium chloride solution (400 mL) in the same buffer. The recombinant loop-modified cellulase of interest was eluted at a sodium chloride solution concentration of approximately 0.25 M and the eluted component was found substantially homogenous as analyzed by electrophoresis. Desalting and condensation were performed through use of an ultrafilter (PM10, Millipore).

Example 5 Optimum reaction pH of recombinant loop-modified cellulase

The purified product of the recombinant loop-modified cellulase prepared in Example 4 was investigated in terms of the effect of pH on enzymatic reaction. Optimum reaction pH was determined by use of glycine-sodium hydroxide buffer (pH 8.2 to 10.9). As a result, a recombinant wild-type cellulase was found to have an optimum reaction pH of 9.0, whereas the cellulase which had been modified by alanine-glycine-alanine was found to have an optimum reaction pH of 10, which is 1 pH

unit higher than that of the recombinant wild-type cellulase (Fig. 2); i.e., the optimum pH shifted toward higher alkaline side. The cellulase, which had been modified by alanine-histidine-alanine or alanine-arginine-alanine was found to have an optimum reaction pH of about 9.6. In addition, within a range of pH 8.8 to pH 9.9, the cellulase which had been modified by alanine-histidine-alanine or alanine-arginine-alanine was found to have a relative activity (i.e., a percent activity when the activity at optimum reaction pH, in this case, pH 9.6, is taken as 100%) of 95% or more, which is higher than those of the parent cellulase and the cellulase mutated by alanine-glycine-alanine (Figs. 2 and 3).

Industrial Applicability

The mutated alkaline cellulases of the present invention have an optimum pH near the pH of the washing liquid (pH of about 10.5), and thus are useful as enzymes for detergents.